

## SEQUENCE LISTING

<110> Yang, Meija

<120> NOVEL THERAPEUTIC FUSION PROTEINS

<130> ARS-121

<140> US 10/566,929

<141> 2006-02-02

<150> US 60/492,397

<151> 2003-08-04

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 183

<212> PRT

<213> Homo sapiens

<400> 1

Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser  
1 5 10 15

Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp  
20 25 30

Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro  
35 40 45

Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln  
50 55 60

Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe  
65 70 75 80

Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu  
85 90 95

Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly  
100 105 110

Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro  
115 120 125

Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys  
130 135 140

Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr  
145 150 155 160

Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly  
                   165                  170                  175

Arg Gly Val Leu Asp Gln Gln  
                   180

<210> 2  
 <211> 661  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile  
 1                  5                  10                  15

Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly  
                   20                  25                  30

Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala  
                   35                  40                  45

Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala  
                   50                  55                  60

Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln  
 65                  70                  75                  80

Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn  
                   85                  90                  95

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro  
                   100                  105                  110

Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val  
                   115                  120                  125

Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala  
                   130                  135                  140

Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe  
 145                  150                  155                  160

Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val  
                   165                  170                  175

Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala  
                   180                  185                  190

Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro  
                   195                  200                  205

Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala

210	215	220
Val Val Ala Arg Ser	Val Asn Gly Lys Glu Asp	Ala Ile Trp Asn Leu
225	230	235 240
Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe		
	245	250 255
Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp		
	260	265 270
Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu		
	275	280 285
Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser		
	290	295 300
Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val		
	305	310 315 320
Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu		
	325	330 335
Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala		
	340	345 350
Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr		
	355	360 365
Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn		
	370	375 380
Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg		
	385	390 395 400
Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr		
	405	410 415
Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala		
	420	425 430
Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn		
	435	440 445
Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala		
	450	455 460
Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp		
	465	470 475 480
Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr		
	485	490 495
Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val		
	500	505 510

Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn  
 515 520 525  
 Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu  
 530 535 540  
 Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His  
 545 550 555 560  
 Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val  
 565 570 575  
 Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg  
 580 585 590  
 Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr  
 595 600 605  
 Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His  
 610 615 620  
 Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly  
 625 630 635 640  
 Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys  
 645 650 655  
 Glu Phe Leu Arg Lys  
 660

<210> 3  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 3

Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser Ser Val Thr  
 1 5 10 15  
 Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met  
 20 25 30  
 Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro  
 35 40 45  
 Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr  
 50 55 60  
 Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu  
 65 70 75 80  
 His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile Trp

85

90

<210> 4  
 <211> 753  
 <212> PRT  
 <213> Artificial sequence

<220>

<223> Lactoferrin / HFE-based recycling domain RC1

<400> 4

Gly	Pro	Pro	Val	Ser	Cys	Ile	Lys	Arg	Asp	Ser	Pro	Ile	Gln	Cys	Ile	1	5	10	15
Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly	Gly	20	25	30	
Phe	Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val	Ala	35	40	45	
Ala	Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr	Ala	50	55	60	
Val	Ala	Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	Leu	Asn	Glu	Leu	Gln	65	70	75	80
Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp	Asn	85	90	95	
Val	Pro	Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro	Pro	100	105	110	
Glu	Pro	Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	Ser	Ala	Ser	Cys	Val	115	120	125	
Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	Ala	130	135	140	
Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	Gln	Glu	Pro	Tyr	Phe	145	150	155	160
Ser	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	Gly	Ala	Gly	Asp	Val	165	170	175	
Ala	Phe	Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	Leu	Ser	Asp	Glu	Ala	180	185	190	
Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	Asn	Thr	Arg	Lys	Pro	195	200	205	
Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	Val	Pro	Ser	His	Ala	210	215	220	

Val	Val	Ala	Arg	Ser	Val	Asn	Gly	Lys	Glu	Asp	Ala	Ile	Trp	Asn	Leu	225	230	235	240
Leu	Arg	Gln	Ala	Gln	Glu	Lys	Phe	Gly	Lys	Asp	Lys	Ser	Pro	Lys	Phe	245	250	255	
Gln	Leu	Phe	Gly	Ser	Pro	Ser	Gly	Gln	Lys	Asp	Leu	Leu	Phe	Lys	Asp	260	265	270	
Ser	Ala	Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg	Ile	Asp	Ser	Gly	Leu	275	280	285	
Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg	Lys	Ser	290	295	300	
Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val	Val	Trp	Cys	Ala	Val	305	310	315	320
Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp	Ser	Gly	Leu	Ser	Glu	325	330	335	
Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr	Glu	Asp	Cys	Ile	Ala	340	345	350	
Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly	Tyr	355	360	365	
Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu	Asn	370	375	380	
Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro	Asn	Cys	Val	Asp	Arg	385	390	395	400
Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser	Asp	Thr	405	410	415	
Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	Ala	420	425	430	
Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Phe	Asn	435	440	445	
Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser	Cys	Ala	450	455	460	
Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile	Gly	Asp	465	470	475	480
Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg	Tyr	Tyr	485	490	495	
Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly	Asp	Val	500	505	510	
Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly	Asn	Asn				

515					520					525					
Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala	Leu	Leu
530						535					540				
Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser	Cys	His
545					550					555					560
Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp	Lys	Val
				565					570					575	
Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	Ala	Lys	Phe	Gly	Arg
			580					585					590		
Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	Phe	Gln	Ser	Glu	Thr
		595					600					605			
Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	Leu	Ala	Arg	Leu	His
	610					615					620				
Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	Gln	Tyr	Val	Ala	Gly
625					630					635					640
Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro	Leu	Leu	Glu	Ala	Cys
				645					650					655	
Glu	Phe	Leu	Arg	Lys	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His	His	Val
			660					665					670		
Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr	Tyr	Pro
		675					680					685			
Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met	Asp	Ala
	690					695					700				
Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly	Thr	Tyr
705					710					715					720
Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln	Arg	Tyr
				725					730					735	
Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile	Val	Ile
			740					745					750		

Trp

<210> 5  
 <211> 275  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Lactoferin / HFE-based recycling domain RC2

&lt;400&gt; 5

Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser  
 1 5 10 15  
 Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp  
 20 25 30  
 Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro  
 35 40 45  
 Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln  
 50 55 60  
 Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe  
 65 70 75 80  
 Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu  
 85 90 95  
 Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly  
 100 105 110  
 Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro  
 115 120 125  
 Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys  
 130 135 140  
 Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr  
 145 150 155 160  
 Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly  
 165 170 175  
 Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His  
 180 185 190  
 His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr  
 195 200 205  
 Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met  
 210 215 220  
 Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly  
 225 230 235 240  
 Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln  
 245 250 255  
 Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile  
 260 265 270  
 Val Ile Trp  
 275



<210> 6  
 <211> 753  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Lactoferin / HFE-based recycling domain RC3

<400> 6

Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His	His	Val	Thr	Ser	Ser	Val	Thr	1	5	10	15
Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr	Tyr	Pro	Gln	Asn	Ile	Thr	Met	20	25	30	
Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met	Asp	Ala	Lys	Glu	Phe	Glu	Pro	35	40	45	
Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly	Thr	Tyr	Gln	Gly	Trp	Ile	Thr	50	55	60	
Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln	Arg	Tyr	Thr	Cys	Gln	Val	Glu	65	70	75	80
His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile	Val	Ile	Trp	Gly	Pro	Pro	Val	85	90	95	
Ser	Cys	Ile	Lys	Arg	Asp	Ser	Pro	Ile	Gln	Cys	Ile	Gln	Ala	Ile	Ala	100	105	110	
Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly	Gly	Phe	Ile	Tyr	Glu	115	120	125	
Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val	Ala	Ala	Glu	Val	Tyr	130	135	140	
Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr	Ala	Val	Ala	Val	Val	145	150	155	160
Lys	Lys	Gly	Gly	Ser	Phe	Gln	Leu	Asn	Glu	Leu	Gln	Gly	Leu	Lys	Ser	165	170	175	
Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp	Asn	Val	Pro	Ile	Gly	180	185	190	
Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro	Pro	Glu	Pro	Ile	Glu	195	200	205	
Ala	Ala	Val	Ala	Arg	Phe	Phe	Ser	Ala	Ser	Cys	Val	Pro	Gly	Ala	Asp	210	215	220	
Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	Ala	Gly	Thr	Gly	Glu				

225		230		235		240
Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser Tyr Ser Gly						
		245		250		255
Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala Phe Ile Arg						
		260		265		270
Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu Arg Asp Glu						
		275		280		285
Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val Asp Lys Phe						
		290		295		300
Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val Val Ala Arg						
		305		310		315
Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu Arg Gln Ala						
		325		330		335
Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln Leu Phe Gly						
		340		345		350
Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser Ala Ile Gly						
		355		360		365
Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr Leu Gly Ser						
		370		375		380
Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu Glu Glu Val						
		385		390		395
Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly Glu Gln Glu						
		405		410		415
Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly Ser Val Thr						
		420		425		430
Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu Val Leu Lys						
		435		440		445
Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val Tyr Thr Ala						
		450		455		460
Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Lys Ser Gln						
		465		470		475
Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro Val Glu Gly						
		485		490		495
Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser Leu Thr Trp						
		500		505		510
Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val Asp Arg Thr						
		515		520		525

Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln Thr Gly Ser  
 530 535 540  
 Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro Gly Ser Asp  
 545 550 555 560  
 Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu Gln Gly Glu  
 565 570 575  
 Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly Tyr Thr Gly  
 580 585 590  
 Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala Phe Val Lys  
 595 600 605  
 Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn Glu Ala Trp  
 610 615 620  
 Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys Leu Asp Gly  
 625 630 635 640  
 Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu Ala Met Ala  
 645 650 655  
 Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu Arg Leu Lys  
 660 665 670  
 Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn Gly Ser Asp  
 675 680 685  
 Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys Asn Leu Leu  
 690 695 700  
 Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly Lys Thr Thr  
 705 710 715 720  
 Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile Thr Asn Leu  
 725 730 735  
 Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu Phe Leu Arg  
 740 745 750

Lys

<210> 7  
 <211> 275  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Lactoferin / HFE-based recycling domain RC4  
  
 <400> 7

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<210> 8  
 <211> 21  
 <212> PRT  
 <213> Mus musculus

<400> 8

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15

Gly Ser Thr Gly Asp  
 20

<210> 9  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 9

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15

Asp Thr Thr Gly  
 20

<210> 10  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln His Ile  
 1 5 10 15

Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala  
 20 25 30

His Lys Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu  
 35 40 45

Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser  
 50 55 60

Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser  
 65 70 75 80

Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser  
 85 90 95

Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met

100	105	110
Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu 115 120 125		
Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys 130 135 140		
Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp 145 150 155 160		
Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile 165 170 175		
Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr 180 185 190		
Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile 195 200 205		
Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val Leu 210 215 220		
Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr Trp 225 230 235 240		
Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile 245 250 255		
Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile 260 265 270		
Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg 275 280 285		
Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His 290 295 300		

<210> 11  
 <211> 1042  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC1(n)VEGF

<400> 11

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro 1 5 10 15
Gly Ser Thr Gly Asp Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser 20 25 30

Pro Ile Gln Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val  
 35 40 45  
 Thr Leu Asp Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys  
 50 55 60  
 Leu Arg Pro Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg  
 65 70 75 80  
 Thr His Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln  
 85 90 95  
 Leu Asn Glu Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg  
 100 105 110  
 Thr Ala Gly Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn  
 115 120 125  
 Trp Thr Gly Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe  
 130 135 140  
 Ser Ala Ser Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu  
 145 150 155 160  
 Cys Arg Leu Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser  
 165 170 175  
 Gln Glu Pro Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp  
 180 185 190  
 Gly Ala Gly Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp  
 195 200 205  
 Leu Ser Asp Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp  
 210 215 220  
 Asn Thr Arg Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg  
 225 230 235 240  
 Val Pro Ser His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp  
 245 250 255  
 Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp  
 260 265 270  
 Lys Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp  
 275 280 285  
 Leu Leu Phe Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg  
 290 295 300  
 Ile Asp Ser Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln  
 305 310 315 320  
 Asn Leu Arg Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val

	325		330		335	
Val Trp Cys	Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp					
	340		345		350	
Ser Gly Leu	Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr					
	355		360		365	
Glu Asp Cys	Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser					
	370		375		380	
Leu Asp Gly	Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro					
	385		390		395	400
Val Leu Ala	Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro					
	405		410		415	
Asn Cys Val	Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val					
	420		425		430	
Arg Arg Ser	Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys					
	435		440		445	
Ser Cys His	Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met					
	450		455		460	
Gly Leu Leu	Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe					
	465		470		475	480
Ser Gln Ser	Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala					
	485		490		495	
Leu Cys Ile	Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser					
	500		505		510	
Asn Glu Arg	Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu					
	515		520		525	
Asn Ala Gly	Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn					
	530		535		540	
Thr Asp Gly	Asn Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala					
	545		550		555	560
Asp Phe Ala	Leu Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu					
	565		570		575	
Ala Arg Ser	Cys His Leu Ala Met Ala Pro Asn His Ala Val Val Ser					
	580		585		590	
Arg Met Asp	Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln					
	595		600		605	
Ala Lys Phe	Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu					
	610		615		620	



Phe Gln Ser Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys  
 625 630 635 640  
 Leu Ala Arg Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro  
 645 650 655  
 Gln Tyr Val Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro  
 660 665 670  
 Leu Leu Glu Ala Cys Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys  
 675 680 685  
 Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala  
 690 695 700  
 Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys  
 705 710 715 720  
 Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn  
 725 730 735  
 Gly Asp Gly Thr Tyr Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys  
 740 745 750  
 Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys  
 755 760 765  
 Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys  
 770 775 780  
 Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly  
 785 790 795 800  
 Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His  
 805 810 815  
 Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys  
 820 825 830  
 Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg  
 835 840 845  
 Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr  
 850 855 860  
 Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile  
 865 870 875 880  
 Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly  
 885 890 895  
 Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala  
 900 905 910

Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly  
 915 920 925  
 His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile  
 930 935 940  
 Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly  
 945 950 955 960  
 His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg  
 965 970 975  
 Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser  
 980 985 990  
 Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr  
 995 1000 1005  
 Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu  
 1010 1015 1020  
 Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn  
 1025 1030 1035  
 Thr Ser Val His  
 1040

<210> 12  
 <211> 597  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC2(n)VEGF

<400> 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Thr Gly Asp Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu  
 20 25 30  
 Phe Met Gly Ala Ser Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala  
 35 40 45  
 Leu Gly Tyr Val Asp Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser  
 50 55 60  
 Arg Arg Val Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser  
 65 70 75 80  
 Gln Met Trp Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met  
 85 90 95

Phe Thr Val Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys  
 100 105 110  
 Glu Ser His Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp  
 115 120 125  
 Asn Ser Thr Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His  
 130 135 140  
 Leu Glu Phe Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg  
 145 150 155 160  
 Ala Trp Pro Thr Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg  
 165 170 175  
 Gln Asn Arg Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln  
 180 185 190  
 Leu Leu Glu Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu  
 195 200 205  
 Val Lys Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys  
 210 215 220  
 Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys  
 225 230 235 240  
 Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu  
 245 250 255  
 Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro  
 260 265 270  
 Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu  
 275 280 285  
 Asp Gln Pro Leu Ile Val Ile Trp Ser Lys Leu Lys Asp Pro Glu Leu  
 290 295 300  
 Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His  
 305 310 315 320  
 Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met  
 325 330 335  
 Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly  
 340 345 350  
 Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln  
 355 360 365  
 Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr  
 370 375 380

Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp  
 385 390 395 400  
 Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile  
 405 410 415  
 His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser  
 420 425 430  
 Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile  
 435 440 445  
 Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile  
 450 455 460  
 Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr  
 465 470 475 480  
 Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr  
 485 490 495  
 Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu  
 500 505 510  
 Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu  
 515 520 525  
 Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys  
 530 535 540  
 Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn  
 545 550 555 560  
 Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys  
 565 570 575  
 Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val  
 580 585 590  
 Asn Thr Ser Val His  
 595

<210> 13  
 <211> 1042  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC1(c) VEGF

<400> 13

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15

Gly Ser Thr Gly Asp Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys  
 20 25 30  
 Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys  
 35 40 45  
 Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys  
 50 55 60  
 Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly  
 65 70 75 80  
 Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His  
 85 90 95  
 Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys  
 100 105 110  
 Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg  
 115 120 125  
 Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr  
 130 135 140  
 Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile  
 145 150 155 160  
 Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly  
 165 170 175  
 Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala  
 180 185 190  
 Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly  
 195 200 205  
 His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile  
 210 215 220  
 Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly  
 225 230 235 240  
 His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg  
 245 250 255  
 Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser  
 260 265 270  
 Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr  
 275 280 285  
 Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr  
 290 295 300

Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser  
 305 310 315 320  
 Val His Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln  
 325 330 335  
 Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp  
 340 345 350  
 Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro  
 355 360 365  
 Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr  
 370 375 380  
 Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu  
 385 390 395 400  
 Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly  
 405 410 415  
 Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly  
 420 425 430  
 Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser  
 435 440 445  
 Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu  
 450 455 460  
 Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro  
 465 470 475 480  
 Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly  
 485 490 495  
 Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp  
 500 505 510  
 Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg  
 515 520 525  
 Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser  
 530 535 540  
 His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp  
 545 550 555 560  
 Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro  
 565 570 575  
 Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe  
 580 585 590  
 Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser

595					600					605					
Gly	Leu	Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg
610					615					620					
Lys	Ser	Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val	Val	Trp	Cys
625					630					635					640
Ala	Val	Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp	Ser	Gly	Leu
				645					650					655	
Ser	Glu	Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr	Glu	Asp	Cys
			660					665					670		
Ile	Ala	Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly
		675					680					685			
Gly	Tyr	Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala
	690					695					700				
Glu	Asn	Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro	Asn	Cys	Val
705					710					715					720
Asp	Arg	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser
				725					730					735	
Asp	Thr	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His
			740					745					750		
Thr	Ala	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu
		755					760					765			
Phe	Asn	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser
	770					775					780				
Cys	Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile
785					790					795					800
Gly	Asp	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg
				805					810					815	
Tyr	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly
			820					825					830		
Asp	Val	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly
		835					840					845			
Asn	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala
		850				855					860				
Leu	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser
865					870					875					880
Cys	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp
				885					890					895	

Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe  
                   900                  905                  910  
 Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser  
                   915                  920                  925  
 Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg  
                   930                  935                  940  
 Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val  
                   945                  950                  955                  960  
 Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu  
                   965                  970                  975  
 Ala Cys Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His  
                   980                  985                  990  
 His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr  
                   995                  1000                  1005  
 Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro  
                   1010                  1015                  1020  
 Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly  
                   1025                  1030                  1035  
 Asp Gly Thr Tyr  
                   1040

<210> 14  
 <211> 597  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC2(c)VEGF

<400> 14

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1                  5                  10                  15  
 Gly Ser Thr Gly Asp Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys  
                   20                  25                  30  
 Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys  
                   35                  40                  45  
 Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys  
                   50                  55                  60  
 Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly



65		70		75		80									
Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	Ala	Gln	Ala	Asn	His
			85					90						95	
Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	Pro	Thr	Ser	Lys	Lys
			100					105					110		
Lys	Glu	Thr	Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	Ser	Asp	Thr	Gly	Arg
		115					120					125			
Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr
	130					135					140				
Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	Thr	Ser	Pro	Asn	Ile
145					150					155					160
Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp	Gly
				165					170					175	
Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala
		180						185					190		
Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly
		195					200					205			
His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg	Gln	Thr	Asn	Thr	Ile
	210					215					220				
Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val	Lys	Leu	Leu	Arg	Gly
225					230					235					240
His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	Pro	Leu	Asn	Thr	Arg
				245					250					255	
Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	Asn	Lys	Arg	Ala	Ser
		260						265					270		
Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	Ala	Asn	Ile	Phe	Tyr
		275					280					285			
Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	Asp	Lys	Gly	Leu	Tyr
	290					295					300				
Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	Ser	Val	Asn	Thr	Ser
305					310					315					320
Val	His	Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly
				325					330					335	
Ala	Ser	Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr
			340					345					350		
Val	Asp	Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	His	Glu	Ser	Arg	Arg	Val
		355					360						365		

Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp  
 370 375 380  
 Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val  
 385 390 395 400  
 Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His  
 405 410 415  
 Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr  
 420 425 430  
 Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe  
 435 440 445  
 Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro  
 450 455 460  
 Thr Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg  
 465 470 475 480  
 Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu  
 485 490 495  
 Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val  
 500 505 510  
 Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu  
 515 520 525  
 Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln  
 530 535 540  
 Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly  
 545 550 555 560  
 Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu  
 565 570 575  
 Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro  
 580 585 590  
 Leu Ile Val Ile Trp  
 595

<210> 15  
 <211> 251  
 <212> PRT  
 <213> Homo sapiens

<400> 15

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser

1	5	10	15
Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys	20	25	30
Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser	35	40	45
Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys	50	55	60
Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp	65	70	75
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp	85	90	95
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly	100	105	110
Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys	115	120	125
His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn	130	135	140
Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu	145	150	155
Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu	165	170	175
Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu	180	185	190
Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys	195	200	205
Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr	210	215	220
Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr	225	230	235
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser	245	250	

&lt;210&gt; 16

&lt;211&gt; 992

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; CFP-RC1(n)TNF

&lt;400&gt; 16

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Thr Gly Asp Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser  
 20 25 30  
 Pro Ile Gln Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val  
 35 40 45  
 Thr Leu Asp Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys  
 50 55 60  
 Leu Arg Pro Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg  
 65 70 75 80  
 Thr His Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln  
 85 90 95  
 Leu Asn Glu Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg  
 100 105 110  
 Thr Ala Gly Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn  
 115 120 125  
 Trp Thr Gly Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe  
 130 135 140  
 Ser Ala Ser Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu  
 145 150 155 160  
 Cys Arg Leu Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser  
 165 170 175  
 Gln Glu Pro Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp  
 180 185 190  
 Gly Ala Gly Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp  
 195 200 205  
 Leu Ser Asp Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp  
 210 215 220  
 Asn Thr Arg Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg  
 225 230 235 240  
 Val Pro Ser His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp  
 245 250 255  
 Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp  
 260 265 270  
 Lys Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp

275					280					285					
Leu	Leu	Phe	Lys	Asp	Ser	Ala	Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg
290					295					300					
Ile	Asp	Ser	Gly	Leu	Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln
305					310					315					320
Asn	Leu	Arg	Lys	Ser	Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val
				325					330					335	
Val	Trp	Cys	Ala	Val	Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp
			340					345					350		
Ser	Gly	Leu	Ser	Glu	Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr
		355					360					365			
Glu	Asp	Cys	Ile	Ala	Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser
	370					375					380				
Leu	Asp	Gly	Gly	Tyr	Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro
385					390					395					400
Val	Leu	Ala	Glu	Asn	Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro
				405					410					415	
Asn	Cys	Val	Asp	Arg	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val
			420					425					430		
Arg	Arg	Ser	Asp	Thr	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys
		435					440					445			
Ser	Cys	His	Thr	Ala	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met
	450					455					460				
Gly	Leu	Leu	Phe	Asn	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe
465					470					475					480
Ser	Gln	Ser	Cys	Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala
				485					490					495	
Leu	Cys	Ile	Gly	Asp	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser
			500					505					510		
Asn	Glu	Arg	Tyr	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu
		515					520					525			
Asn	Ala	Gly	Asp	Val	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn
	530					535					540				
Thr	Asp	Gly	Asn	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala
545					550					555					560
Asp	Phe	Ala	Leu	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu
				565					570					575	

Ala	Arg	Ser	Cys	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	580	585	590
Arg	Met	Asp	Lys	Val	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	595	600	605
Ala	Lys	Phe	Gly	Arg	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	610	615	620
Phe	Gln	Ser	Glu	Thr	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	625	630	635
Leu	Ala	Arg	Leu	His	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	645	650	655
Gln	Tyr	Val	Ala	Gly	Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro	660	665	670
Leu	Leu	Glu	Ala	Cys	Glu	Phe	Leu	Arg	Lys	Val	Pro	Pro	Leu	Val	Lys	675	680	685
Val	Thr	His	His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	690	695	700
Leu	Asn	Tyr	Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	705	710	715
Gln	Pro	Met	Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	725	730	735
Gly	Asp	Gly	Thr	Tyr	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	740	745	750
Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	755	760	765
Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	770	775	780
Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	785	790	795
Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	805	810	815
Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	820	825	830
Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	835	840	845
Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	850	855	860

Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys  
865 870 875 880

Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys  
885 890 895

Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
900 905 910

Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu  
915 920 925

Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu  
930 935 940

Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu  
945 950 955 960

Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro  
965 970 975

Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser  
980 985 990

<210> 17

<211> 547

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(n)TNF

<400> 17

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Asp Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu  
20 25 30

Phe Met Gly Ala Ser Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala  
35 40 45

Leu Gly Tyr Val Asp Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser  
50 55 60

Arg Arg Val Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser  
65 70 75 80

Gln Met Trp Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met  
85 90 95

Phe Thr Val Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys  
100 105 110

Glu Ser His Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp  
 115 120 125  
 Asn Ser Thr Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His  
 130 135 140  
 Leu Glu Phe Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg  
 145 150 155 160  
 Ala Trp Pro Thr Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg  
 165 170 175  
 Gln Asn Arg Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln  
 180 185 190  
 Leu Leu Glu Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu  
 195 200 205  
 Val Lys Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys  
 210 215 220  
 Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys  
 225 230 235 240  
 Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu  
 245 250 255  
 Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro  
 260 265 270  
 Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu  
 275 280 285  
 Asp Gln Pro Leu Ile Val Ile Trp Asp Ser Val Cys Pro Gln Gly Lys  
 290 295 300  
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 305 310 315 320  
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 325 330 335  
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 340 345 350  
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 355 360 365  
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 370 375 380  
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 385 390 395 400



Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 405 410 415  
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 420 425 430  
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 435 440 445  
 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
 450 455 460  
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 465 470 475 480  
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 485 490 495  
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 500 505 510  
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 515 520 525  
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
 530 535 540  
 Pro Ser Ser  
 545

<210> 18  
 <211> 992  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC1(c)TNF

<400> 18

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Thr Gly Asp Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His  
 20 25 30  
 Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr  
 35 40 45  
 Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu  
 50 55 60  
 Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys  
 65 70 75 80

Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser  
 85 90 95  
 Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln  
 100 105 110  
 Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser  
 115 120 125  
 Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn  
 130 135 140  
 Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys  
 145 150 155 160  
 Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys  
 165 170 175  
 Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
 180 185 190  
 Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu  
 195 200 205  
 Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu  
 210 215 220  
 Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu  
 225 230 235 240  
 Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro  
 245 250 255  
 Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser  
 260 265 270  
 Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile  
 275 280 285  
 Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly  
 290 295 300  
 Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala  
 305 310 315 320  
 Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala  
 325 330 335  
 Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln  
 340 345 350  
 Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn  
 355 360 365

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro  
 370 375 380  
 Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val  
 385 390 395 400  
 Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala  
 405 410 415  
 Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe  
 420 425 430  
 Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val  
 435 440 445  
 Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala  
 450 455 460  
 Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro  
 465 470 475 480  
 Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala  
 485 490 495  
 Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu  
 500 505 510  
 Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe  
 515 520 525  
 Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp  
 530 535 540  
 Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu  
 545 550 555 560  
 Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser  
 565 570 575  
 Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val  
 580 585 590  
 Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu  
 595 600 605  
 Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala  
 610 615 620  
 Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr  
 625 630 635 640  
 Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn  
 645 650 655  
 Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg

660	665	670
Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr 675 680 685		
Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala 690 695 700		
Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn 705 710 715 720		
Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala 725 730 735		
Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp 740 745 750		
Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr 755 760 765		
Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val 770 775 780		
Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn 785 790 795 800		
Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu 805 810 815		
Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His 820 825 830		
Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val 835 840 845		
Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg 850 855 860		
Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr 865 870 875 880		
Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His 885 890 895		
Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly 900 905 910		
Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys 915 920 925		
Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His His Val 930 935 940		
Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro 945 950 955 960		

Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala  
                           965                          970                          975

Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr  
                           980                          985                          990

<210> 19

<211> 547

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(c)TNF

<400> 19

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
   1                          5                          10                          15

Gly Ser Thr Gly Asp Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His  
                           20                          25                          30

Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr  
                           35                          40                          45

Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu  
                           50                          55                          60

Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys  
   65                          70                          75                          80

Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser  
                           85                          90                          95

Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln  
                           100                          105                          110

Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser  
                           115                          120                          125

Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn  
                           130                          135                          140

Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys  
   145                          150                          155                          160

Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys  
                           165                          170                          175

Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
                           180                          185                          190

Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu

195					200					205					
Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	Ser	Lys	Leu
210						215					220				
Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	Gly	Glu	Leu
225					230					235					240
Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	Phe	Ser	Pro
				245					250					255	
Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val	Pro	Ser	Ser
			260					265					270		
Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly	Ala	Ser
		275					280					285			
Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr	Val	Asp
		290				295					300				
Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	His	Glu	Ser	Arg	Arg	Val	Glu	Pro
305					310					315					320
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
				325					330					335	
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
			340					345					350		
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	His	Ser	Lys	Glu	Ser	His	Thr	Leu
		355					360					365			
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
	370					375					380				
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	His	Leu	Glu	Phe	Cys	Pro
385					390					395					400
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
				405					410					415	
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
			420					425					430		
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly
		435					440					445			
Arg	Gly	Val	Leu	Asp	Gln	Gln	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His
	450					455					460				
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr
465					470					475					480
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met
				485					490					495	

Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly  
 500 505 510

Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln  
 515 520 525

Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile  
 530 535 540

Val Ile Trp  
 545

<210> 20  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

<400> 20

Thr Pro Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser  
 1 5 10 15

Thr Lys Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys  
 20 25 30

Gln Cys Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu  
 35 40 45

Asn Gly Thr Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn  
 50 55 60

Phe Ser Ile Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu  
 65 70 75 80

Pro Gly Arg Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr  
 85 90 95

Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala  
 100 105 110

Leu His Ser Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val  
 115 120 125

Val Gln Arg His Val Val Leu Ala Gln Leu Trp Val Arg Ser Pro Arg  
 130 135 140

Arg Gly Leu Gln Glu Gln Glu Leu Cys Phe His Met Trp Gly Gly  
 145 150 155 160

Lys Gly Gly Leu Cys Gln Ser Ser Leu  
 165

<210> 21  
 <211> 910  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC1(n)IL18

<400> 21

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	1	5	10	15
Gly	Ser	Thr	Gly	Asp	Gly	Pro	Pro	Val	Ser	Cys	Ile	Lys	Arg	Asp	Ser	20	25	30	
Pro	Ile	Gln	Cys	Ile	Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	35	40	45	
Thr	Leu	Asp	Gly	Gly	Phe	Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	50	55	60	
Leu	Arg	Pro	Val	Ala	Ala	Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	65	70	75	80
Thr	His	Tyr	Tyr	Ala	Val	Ala	Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	85	90	95	
Leu	Asn	Glu	Leu	Gln	Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	100	105	110	
Thr	Ala	Gly	Trp	Asn	Val	Pro	Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	115	120	125	
Trp	Thr	Gly	Pro	Pro	Glu	Pro	Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	130	135	140	
Ser	Ala	Ser	Cys	Val	Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	145	150	155	160
Cys	Arg	Leu	Cys	Ala	Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	165	170	175	
Gln	Glu	Pro	Tyr	Phe	Ser	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	180	185	190	
Gly	Ala	Gly	Asp	Val	Ala	Phe	Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	195	200	205	
Leu	Ser	Asp	Glu	Ala	Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	210	215	220	
Asn	Thr	Arg	Lys	Pro	Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	225	230	235	240



Val Pro Ser His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp  
 245 250 255  
 Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp  
 260 265 270  
 Lys Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp  
 275 280 285  
 Leu Leu Phe Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg  
 290 295 300  
 Ile Asp Ser Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln  
 305 310 315 320  
 Asn Leu Arg Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val  
 325 330 335  
 Val Trp Cys Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp  
 340 345 350  
 Ser Gly Leu Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr  
 355 360 365  
 Glu Asp Cys Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser  
 370 375 380  
 Leu Asp Gly Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro  
 385 390 395 400  
 Val Leu Ala Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro  
 405 410 415  
 Asn Cys Val Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val  
 420 425 430  
 Arg Arg Ser Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys  
 435 440 445  
 Ser Cys His Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met  
 450 455 460  
 Gly Leu Leu Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe  
 465 470 475 480  
 Ser Gln Ser Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala  
 485 490 495  
 Leu Cys Ile Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser  
 500 505 510  
 Asn Glu Arg Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu  
 515 520 525  
 Asn Ala Gly Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn

530					535					540					
Thr	Asp	Gly	Asn	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala
545					550					555					560
Asp	Phe	Ala	Leu	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu
				565					570					575	
Ala	Arg	Ser	Cys	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser
			580					585					590		
Arg	Met	Asp	Lys	Val	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln
		595					600					605			
Ala	Lys	Phe	Gly	Arg	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu
	610					615					620				
Phe	Gln	Ser	Glu	Thr	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys
625					630					635					640
Leu	Ala	Arg	Leu	His	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro
				645					650					655	
Gln	Tyr	Val	Ala	Gly	Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro
			660					665					670		
Leu	Leu	Glu	Ala	Cys	Glu	Phe	Leu	Arg	Lys	Val	Pro	Pro	Leu	Val	Lys
		675					680					685			
Val	Thr	His	His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala
	690					695					700				
Leu	Asn	Tyr	Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys
705					710					715					720
Gln	Pro	Met	Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn
				725					730					735	
Gly	Asp	Gly	Thr	Tyr	Thr	Pro	Val	Ser	Gln	Thr	Thr	Thr	Ala	Ala	Thr
			740					745					750		
Ala	Ser	Val	Arg	Ser	Thr	Lys	Asp	Pro	Cys	Pro	Ser	Gln	Pro	Pro	Val
		755					760					765			
Phe	Pro	Ala	Ala	Lys	Gln	Cys	Pro	Ala	Leu	Glu	Val	Thr	Trp	Pro	Glu
	770					775					780				
Val	Glu	Val	Pro	Leu	Asn	Gly	Thr	Leu	Ser	Leu	Ser	Cys	Val	Ala	Cys
785					790					795					800
Ser	Arg	Phe	Pro	Asn	Phe	Ser	Ile	Leu	Tyr	Trp	Leu	Gly	Asn	Gly	Ser
				805					810					815	
Phe	Ile	Glu	His	Leu	Pro	Gly	Arg	Leu	Trp	Glu	Gly	Ser	Thr	Ser	Arg
			820					825					830		

Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu  
835 840 845

Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys Val Leu Val  
850 855 860

Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala Gln Leu Trp  
865 870 875 880

Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu Leu Cys Phe  
885 890 895

His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser Leu  
900 905 910

<210> 22

<211> 465

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(n) IL18

<400> 22

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Asp Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu  
20 25 30

Phe Met Gly Ala Ser Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala  
35 40 45

Leu Gly Tyr Val Asp Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser  
50 55 60

Arg Arg Val Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser  
65 70 75 80

Gln Met Trp Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met  
85 90 95

Phe Thr Val Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys  
100 105 110

Glu Ser His Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp  
115 120 125

Asn Ser Thr Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His  
130 135 140

Leu Glu Phe Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg

145		150		155		160
Ala Trp Pro Thr	Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg					
	165			170		175
Gln Asn Arg Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln						
	180			185		190
Leu Leu Glu Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu						
	195			200		205
Val Lys Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys						
	210			215		220
Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys						
	225			230		240
Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu						
	245			250		255
Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro						
	260			265		270
Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu						
	275			280		285
Asp Gln Pro Leu Ile Val Ile Trp Thr Pro Val Ser Gln Thr Thr Thr						
	290			295		300
Ala Ala Thr Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln						
	305			310		315
Pro Pro Val Phe Pro Ala Ala Lys Gln Cys Pro Ala Leu Glu Val Thr						
	325			330		335
Trp Pro Glu Val Glu Val Pro Leu Asn Gly Thr Leu Ser Leu Ser Cys						
	340			345		350
Val Ala Cys Ser Arg Phe Pro Asn Phe Ser Ile Leu Tyr Trp Leu Gly						
	355			360		365
Asn Gly Ser Phe Ile Glu His Leu Pro Gly Arg Leu Trp Glu Gly Ser						
	370			375		380
Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu						
	385			390		395
Val Leu Glu Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys						
	405			410		415
Val Leu Val Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala						
	420			425		430
Gln Leu Trp Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu						
	435			440		445

Leu Cys Phe His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser  
 450 455 460

Leu  
 465

<210> 23  
 <211> 910  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> CFP-RC1(c)IL18

<400> 23

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15

Gly Ser Thr Gly Asp Thr Pro Val Ser Gln Thr Thr Thr Ala Ala Thr  
 20 25 30

Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln Pro Pro Val  
 35 40 45

Phe Pro Ala Ala Lys Gln Cys Pro Ala Leu Glu Val Thr Trp Pro Glu  
 50 55 60

Val Glu Val Pro Leu Asn Gly Thr Leu Ser Leu Ser Cys Val Ala Cys  
 65 70 75 80

Ser Arg Phe Pro Asn Phe Ser Ile Leu Tyr Trp Leu Gly Asn Gly Ser  
 85 90 95

Phe Ile Glu His Leu Pro Gly Arg Leu Trp Glu Gly Ser Thr Ser Arg  
 100 105 110

Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu  
 115 120 125

Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys Val Leu Val  
 130 135 140

Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala Gln Leu Trp  
 145 150 155 160

Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu Leu Cys Phe  
 165 170 175

His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser Leu Gly Pro  
 180 185 190

Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln Ala

195	200	205
Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly Phe Ile 210 215 220		
Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala Ala Glu 225 230 235 240		
Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val Ala 245 250 255		
Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly Leu 260 265 270		
Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val Pro 275 280 285		
Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu Pro 290 295 300		
Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro Gly 305 310 315 320		
Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly Thr 325 330 335		
Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser Tyr 340 345 350		
Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala Phe 355 360 365		
Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu Arg 370 375 380		
Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val Asp 385 390 395 400		
Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val Val 405 410 415		
Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu Arg 420 425 430		
Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln Leu 435 440 445		
Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser Ala 450 455 460		
Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr Leu 465 470 475 480		
Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu Glu 485 490 495		

Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly Glu  
                   500                                  505                                  510

Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly Ser  
                   515                                  520                                  525

Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu Val  
                   530                                  535                                  540

Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val Tyr  
 545                                  550                                  555                                  560

Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Lys  
                                   565                                  570                                  575

Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro Val  
                                   580                                  585                                  590

Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser Leu  
                   595                                  600                                  605

Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val Asp  
                   610                                  615                                  620

Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln Thr  
 625                                  630                                  635                                  640

Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro Gly  
                                   645                                  650                                  655

Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu Gln  
                                   660                                  665                                  670

Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly Tyr  
                   675                                  680                                  685

Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala Phe  
                   690                                  695                                  700

Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn Glu  
 705                                  710                                  715                                  720

Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys Leu  
                                   725                                  730                                  735

Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu Ala  
                                   740                                  745                                  750

Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu Arg  
                   755                                  760                                  765

Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn Gly  
                   770                                  775                                  780

Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys Asn  
785 790 795 800

Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly Lys  
805 810 815

Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile Thr  
820 825 830

Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu Phe  
835 840 845

Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser  
850 855 860

Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn  
865 870 875 880

Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala Lys Glu  
885 890 895

Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr  
900 905 910

<210> 24

<211> 465

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(c)IL18

<400> 24

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Asp Thr Pro Val Ser Gln Thr Thr Thr Ala Ala Thr  
20 25 30

Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln Pro Pro Val  
35 40 45

Phe Pro Ala Ala Lys Gln Cys Pro Ala Leu Glu Val Thr Trp Pro Glu  
50 55 60

Val Glu Val Pro Leu Asn Gly Thr Leu Ser Leu Ser Cys Val Ala Cys  
65 70 75 80

Ser Arg Phe Pro Asn Phe Ser Ile Leu Tyr Trp Leu Gly Asn Gly Ser  
85 90 95

Phe Ile Glu His Leu Pro Gly Arg Leu Trp Glu Gly Ser Thr Ser Arg  
100 105 110



Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu  
 115 120 125  
 Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys Val Leu Val  
 130 135 140  
 Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala Gln Leu Trp  
 145 150 155 160  
 Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu Leu Cys Phe  
 165 170 175  
 His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser Leu Arg Leu  
 180 185 190  
 Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser Glu Gln  
 195 200 205  
 Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp Asp Gln  
 210 215 220  
 Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro Arg Thr  
 225 230 235 240  
 Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln Leu Ser  
 245 250 255  
 Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe Trp Thr  
 260 265 270  
 Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu Gln Val  
 275 280 285  
 Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly Tyr Trp  
 290 295 300  
 Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro Asp Thr  
 305 310 315 320  
 Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys Leu Glu  
 325 330 335  
 Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr Leu Glu  
 340 345 350  
 Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly Arg Gly  
 355 360 365  
 Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His His Val  
 370 375 380  
 Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro  
 385 390 395 400

Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala  
405 410 415

Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr  
420 425 430

Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr  
435 440 445

Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile  
450 455 460

Trp  
465